

## FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC  
TGTGCCCCGGGCTTGGAATTCGCTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT  
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC  
GTTTGGCCCAGGACGGGGCCCATGTGGTCGT CAGCAGCCGGAAGCAGCAGAATGTGGACCAG  
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA  
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC  
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG  
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC  
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC  
CATCTCCTGGCTTCAGTCTTTACAATGTCAGTAAACAGCCTTGCTGGGCCTGACCAAGACC  
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA  
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC  
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCTGTGCTCT  
GAAGATGCCAGCTACATCACTGGGGAAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT  
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGTGTCTCCTGC  
ATTCACCCACCTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT  
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTGTGCT  
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT  
GAGTCTACCTTGGCAAAGACCAAGATATTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA  
TGGGAGAGAAGGAACCTGGAGTGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG  
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

## FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS  
SRKQQNVQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG  
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGGSVVIVSSIAAFSPSPGFSPYNVSK  
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEEESMKETLRIRRLGEPEDC  
AGIVSFLCSEDASYITGETVVVGGGTPSRL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-15

#### **N-glycosylation site.**

amino acids 183-186

#### **N-myristoylation sites.**

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

#### **Microbodies C-terminal targeting signal.**

amino acids 276-278

## FIGURE 3

GCGCCCTGAGCTCCGCCCTCCGGGCCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGCGGGC  
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAAGGTGGC  
GCGGCTGGAGGAGGAGAACCAGAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAAAATGCG  
AGAGCGACCCGCTGCGTGGCAGCAGGAGGAGATGGTGAACCTGCGGTAGAGCTGGTGGCGG  
CCAGGCTGGGGGGGCTGCGGCTCCTGGAATGGCCTGCCTCCCGGGTCTTTGTGCCCTCGACCTCATAC  
AGCCCCCTGGGGGGTGCCACGCCCCATGTGCTGGGCATGGTGCCGCTGCTGCTCCTCGGAGATG  
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT  
GAGGTGAACAGGCTGGGAAGTGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGCTGGCGGC  
CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGACGCCCAG  
GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTTGCCCTGAGGAGTTGGATGCAGCCATTCCAGGGTCC  
AGAGCAGTTGGTGGGAGCAAGGCCGAGTTCAGGCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG  
GCGGCTGGCCAGGCCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA  
TTGGCGAGCTGGTCCGCACAGGAAAGCGAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG  
GAGCTGGAGCAGGAGGCGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCGAGCTGCGGGAGCT  
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGCTCGGCTCCAGGAGTTCGCCAGGAGGGTTCGCTG  
CGGCCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTGCG  
GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATCGGCAGCAGCAGGGACA  
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCCCTGGAGGCAGAAATGAGCAAGCGGC  
AGCACCCGCTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAAGCCGAA  
GAGATCGCGGCTTCCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAAGCTGGAAACAGCA  
GCAGAAGATTGAGGAGCAGAAGAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG  
CGCTGAGAGAGCTGGGGGAGGAGTCCACAAGCGGGAGGCCATCTGGCCCAAGAAGAGGCGCTGATG  
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG  
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA  
GCGCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGTGCTC  
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGTGTCGCCCGAGGAGGAGCGGGAC  
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA  
CATGCCGCCAGCGGGTGCTTCGGGCCCTCAGCCTCGTTGCTGTCCCAGTGCGAGATGAACCTCATGGCC  
AAGCTCAGCTACTCTCATCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC  
GCTCCGAGAGGAGCAGCACCCAGCAGCAGATTGCCCTTCTCGGAAGTGGAGATGCAGCTGGAGGAGCAGC  
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCTGGAGATGGACCCGACCTGACC  
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA  
AGGGTTAGCAGACAGCAGGAGGCGAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAAGTGGGCCGTT  
ACATGTGGATAAACAGGAAGTGAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT  
GGGAGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAATGAAGATGAGCTCCACCTGGC  
ACCGGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGCGCGGGACT  
TGGTCCACGCTCCGTTACCTTACCTGGAACGCTCGAGCCTGTGTGGTGGAGGAGCAGGGTCCCC  
GAGGAAGTGAAGCAGCGGGAGGCGGCTGAGCCCTGGTGGGGCGGGTCTTCTGTGGGTGAGGCAGG  
CCTGCCCTGGAACCTTTGGGCTTTGTCCAAGCCCCGGCGGAACTGCGACGAGCCAGCCCGGGGATGA  
TTGATGTCGGGAAAAACCCCTCTGAAGCCCTCGGGGCAGACCCTGCCTTGGAGGGAGACTCCGAGCCT  
GCTGAAAGGGGCGAGCTGCCGTGTTTGTCTCTGTGAAGGGCAGTCTTACCGCACACCTTAATCCAGG  
CCCTCATCTGTACCTCACTGGGATCAACAAATTTGGGCCATGGCCCCAAAAGAACTGGACCCTATT  
AACAAAATAATATGCAAAATCCCACCATTACTTCCATGAAGCTGAGTGTGAGTACCAATGGCGGCTGTG  
TCTTGCTCGAATCTCAGGACAATTCTGTTTCAGGCGTAATGATGTGCTGTGAGTTGAGGCTGGTTG  
GCCAAGAATCATCACGAAAGGGTGGTGGCAACCAGGTTGTGGTTAAATGGTCTTATGTATATAGG  
GAAACTGGGAGACTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

## **FIGURE 4**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKQLQSDRLREQQEEMVELRLRLELVRPGWGGLRLNLGLPPGSFVPRPHTAPLGGAHAV  
LGMVPPACLPGLDEVGSEQRGEQVTNGREAGAEELLTEVNRLGSGSSAASEEEEEEEPPRRTL  
HLRRNRISNCSQRAGARPGSLPERKGPCLCLEELDAAIPGSRAVGGSKARVQARQVPPATAS  
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE  
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVLSAQSEKRLQE  
LERNVQLMRQQQQLQRRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA  
AFQKRRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQRRALEELGEELHKREAILAKKE  
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSQAQSQQQIRGEIDS  
LRQEKDSLKQRLIEDGKLRQGSLLSPBEERTLFLQLEAIEALDAAIEYKNEAITCRQRVLR  
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR  
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGADSRQYEARIQALEK  
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG  
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG  
PLSKPRRELRRASPGMIDVRKNPL

**Important features:**

**Leucine zipper pattern.**

amino acids 557-579, 794-815

**N-glycosylation sites.**

amino acids 133-136, 383-386

**Kinesin related protein Kif-4 Coiled-coil domain:**

amino acids 231-672

## **FIGURE 5**

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT  
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA  
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCTTCAGAGCAGTG  
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT  
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTG  
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCCGGAGCTGTAC  
CAGGAACAGGAGGCACGTCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC  
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA  
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTTGGAGAGGAGCCCAGCTGGGGATGGC  
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTCCAGCTCCCCTTCCCGCTGAG  
AGCCACTTTCATCGGCAATAAAATCCCCACATTTACCATCT

LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPI SRSCTRNRRHVLYP

amino acids 33-39, 70-76

## FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGTCCGGGCTTCTCT  
TTTCCTCCGACGCGCCACGGCTGCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG  
AACCCCTCCGCGAGAGGAGCGAGGCGGCCAGGGTGGCCCCCGGGGCGCGTCTGGTCTCG  
GAGAAAGCGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT  
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCAGAGACGCCCTAGCCCC  
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG  
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCGGGCCCGCGCCCGCGCTGCTACCCCTG  
CGCCCGCTGCGAGCCCGGCGTCCGGCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG  
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCTCGGCCGCGCTCCCCGCCCGCCC  
GCCCGCCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA  
GTTCCCTCCTGGTACCTGCTGCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG  
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG  
CCCGGGGCGGGTGAACGAGCTCGGGCGCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT  
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC  
TGGGTCTCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCGGGCCCGCGGGGACAC  
CCCGCAGGCGGAAGCCCTGGCCGAGCCGCCAGGACGCGATTGGCCCGGAACTCGCGCCCA  
CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG  
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTGCGCGCGGGCCCCCTCGGCCTGCCCGTGCCT  
GTGCACCGAGGAGGGGCCGCTGTGCGCGCAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCA  
TCCACGTCGACACGAGCCAGTGCTGCCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC  
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGCTCCATGCGAGAGGTGTCGCTG  
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGACGCTGTCCCAGACGGAGTGTGTGGACC  
CTGTGTACGAGCCTGATCAGTGCTGTCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAA  
ACCGCGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGCAACCATATGCCACTGTAC  
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC  
AAATGAGACGCTTCCCGAACAACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA  
CATTCTAGATGACTCTGGGAATATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA  
TTGTTGGTACTTTTCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT  
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG  
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG  
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AAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818  
><subunit 1 of 1, 325 aa, 1 stop  
><MW: 35296, pI: 5.37, NX(S/T): 0  
MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL  
GRPARDEGGSGRDWKS KSGRGLAGREFWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALA  
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDESGFVYAIGKEKFAPGPSACPLCTEEGPL  
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVS PCERCRCCEANGEVL  
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETA V I PAGREVKTDECTICHCTYEEGTWR  
IERQAMCTRHECRQM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187



## FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC  
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
CACGTTGATGCTCATTTAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGGTGCACGG  
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
AAGGTGTCTGAGGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA  
ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGACCACCATTATGACACACGGAAAC  
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG  
GCTGCAGCACTGTTGGGGCTCAAAAATTTCCAGAAGACCACCATCCACTCAGCCCTCCTGGG  
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTC  
CTACCTGTGTGCAGCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
GGCGCCACTCATTTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT  
GAGCATTCAAGGCTGCGTGGCCCAACCTTCAGCTTCTTGTGAACCACACCAGACAAATCG  
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
GTGGGGAGTGGTTTGCCTTCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
CCACCACACTCAACCTCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTTC  
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCTATCTACTCACCTAACAGCA  
ACACTGGGGAGAGCCTGGAGCATCCGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
GCTGCATGTATCTGATAATACAGACCTGTCTTTCA

## **FIGURE 10**

```
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><subunit 1 of 1, 437 aa, 1 stop
><MW: 46363, pI: 6.22, NX(S/T): 3
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ESGPQVSVLSKSGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGFVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVCPSC
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 243-260

**N-glycosylation sites.**

amino acids 46-49, 189-192, 382-385

**Glycosaminoglycan attachment sites.**

amino acids 51-54, 359-362

**N-myristoylation sites.**

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,  
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,  
360-365, 361-366, 388-393, 408-413, 419-424

## FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG  
GCTGCGCGCTGCTCTCTCGCTTGGCGCTGCTCTCTTAGAGCCGAGGGACCCGGTGGC  
CTCGTCGCTCAGCCCCATTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT  
TGTGCGGCCCGGAGGCTCCGTGGCGGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG  
CAGCTGGTCGCCTCATTCGCCACGGCACC CGCTACCCACGGTCAAACAGATCCGCAAGCT  
GAGGCGAGCTGCACGGGTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGCTAGTAGTACCG  
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC  
GGGCGAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT  
CTTCCC GGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACAGTTCCAAGC  
ACCGCTGCATGGATAGCAGCGCCGCTTCTTCGAGGGGCTGTGGCAGCACTACCACCCTGGC  
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GAGATTTTTTGATCACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTT  
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ACTATTAAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGC  
AGTTGAACAGAAACAAAGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG  
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA  
CGGTACAAATTACAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTTGATACCTTATGC  
CTCGAACCTGATATTTGTGCTTTTACCCTGTGAAAATGCTAAGACTCCTAAAGAACAATTCC  
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TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAGTACAA  
TGAAAAATAAATATTTTGGTATTTTATGAAATATTGAAACATTTTTCAATAAATCTTT  
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC  
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTCATTCTGT  
CACTTGCTTCGATTTTTATATTTTCTATTATATGAAATGTATCTTTGGTTGTTTGATT  
TTCTTTCTTTCTTTGTAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA  
TAAAGAAAATCTTGTGACTTTAAAAA

## FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

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GPEAPWRDPELLEGTCTPVLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS  
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR  
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH  
VEAFKGTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEFDLAIKGVKSPWCDVFDIDDA  
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE  
TLLPLLSLMGYFKDKEPLTAYNKKQMHRKFRSGLIVPYASNLIFVLYHCENAKTPKEQFRV  
QMLLNEKVLPLAYSQETVVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

### **Important features:**

#### **Signal sequence**

amino acids 1-30

#### **N-glycosylation sites.**

amino acids 242-246, 481-485

#### **N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

#### **Endoplasmic reticulum targeting sequence.**

amino acids 484-489

10032990.122701

GGGACTACAAGCCGCGCGCGCTGCGCGCTGGCCCCCTCAGCAACCTCGACATGGCGCTGAGGCGGGCCACCGGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTCTCTTCTGCTGCTCTGTTTCAAGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAACTCAGCAATCGAACCCGAGTGGTACAGGAATTTGAAAGTGTGGAACTGTCTTGTCATCATTCAGGATTCG  
AGACAAGTGACCCAGGATCGAGTGGGAAGAAATTCAGATGAACAAACACATATGTGTTTTTGACACAAAA  
TTCCAGGAGCAATCTGGCGGGTGTGCGAGAATACTGGGAAGACATCCCTGAAGATCTGGAATGTGCACGGGAG  
ACTCAGCCCTTATTCGCTGTAGGTCGTGCTCGAAATGACCGCAAGGAATGTAGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAAGCCAGTGACCCCTGTCTGTAGAGTGCAGGAAGCTGTACCACTAGGCAGAGTGGCAACACTGC  
ACTGCCAGGAGATGGGGCCACCCCGGCTCTACTACAGCTGTGATCGCAATGATGTACCACTGCCACGGATT  
CCAGGACCAATCCAGAAITTCGAATCTCTTCTTCCACTTAAATCTGAAACAGGCACTTTGGTGTCTACTGCT  
TTCAAGAAGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGAGGCTCAGCCAGGTGTAGGAGCAGG  
AGATGGAAAGTCTATGACCTGCAACTTGGCGGAATTTATGGGGGGGTCTGGTGTCTGTACTGTGCCCTGTA  
TCAGTTTGGGCACTTCGCTGTGCATACAGACGTGGCTACTCATCAAACTTAACCGATTGGAGAAGTTACAAGA  
ACCCAGGGAAACAGGATGGAGTTAACTACATCCGCACTGACGAGGAGGGGCATTTACAGACAAGATCTGCTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCCAGCTGCACATCCTCTGTTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGCGTAGACATCATTCAGAGCTTTCTGTTTGGCCAAAGTTGACCA  
CTACTCTTCTACTCTAACAGCCACATGAATAGAAGAATTTTCTCTCAAGATGGAACCCGGTAAATATAACCACAA  
GGAGCGAAACTGGGTGGTCTCAGTGATTGGGTTCTTCTGCTTTTGGCCCTGATTCCGCGCATAGGATTAGT  
GTGATTTAAAGAGTTTGCTTCAGTTAAAGCCCGTGCTGGGCCCTGTGAAGCCAGCATCTCCGCACTAGCTGTG  
CAGCAGCCAGCACAGCACCATTGTGAGATGGCAGGTGGCTGGACAGCACCAGCAGCGCATCCGCGCGGGAAACCA  
GAAAGAGCTTCTTACACAGCAGCTCTTACTTCATCGGCCCAACAGACACACCCGAGCTTTCTTCTTAAAGGCTCTGC  
TGATCGTGTTGAGAGTGTCATTGTGGAGAAGTTTGTGATCAGCAATTTGTA AAAACACAAATAACAGGAAG  
GTAATTTGGTGTGTAAGAGGGATCTTGCTGTGAGGAACCTTGCTTGTTCAACAGGGTGTGAGGATTAAAGAAA  
ACCTTGCTCTTAGGCTAAGTGTGAATAGGTACTGAAATATGCTTTTCTATGGGCTGTGTTTATTTATAAAATTT  
TACATCTAAATTTTTCCTAAGGATGTATTTGATTTGAAAGAAATTTCTATTTAAACTGTAAATATATTGT  
CATACAATGTATAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTCCAAGCTACTAGTGTAAAT  
TGAGAAAATATCAATATTAAGAGTTTATACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTCTTTCT  
CAGACAAGTTTATGCTTTTGTCTTCAAGGGAACATCATACTGTACACATCAGACAGTATGTGCTTAGGAACCTT  
TAAAAATTCAGTTTAAGCAATGTGAATTCAGTTTGCATCTTCAAAGAAACCTCTCAGGTTAGCTTTGAATC  
GCTCTTCTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGAGTG  
CCAGTCAGCTCTCTGGGTTGCGCCAGGCGCCCGCTAGCTCATGCTGTGCTGCTGTCTGCGAGGAGCCCT  
GCCATCTTGGGCGCTCGGGAGTGGCTGTGTCCAGTGAGCTTTACTCATGCTGGCCCTTGCTTCACTCCAGACGC  
TCTCAGGTGGCCCTGCAGGACATGGTGTCTTCCATGTAGCGTCCCAGTCTTGGGCTCCTGTAAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAATAATGGGCCCCAATGCTATTTTTTTTTAAGTTTGTTAATATTGTGT  
AAGATTGTCTAAGGCCAAAGGCAATTTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAGAGAAATGGAT  
CCGACTGTCTCTCTTTGCGCAGAGAAAGCCAGCGCCACAGGCTCTGTGCAATTTCAAAGCAAACCATGAT  
GGATGTGCGCGCAGTCCAGCTTTTAAAGAACGCTCAGGTGGAGCAGCAGGTGAAAGGCTTGGCGGGGAGGAAG  
TGAAACGCCGTGAATCAAAGCAGTTTCTTAATTTTGACTTTAAATTTTCTCGCGCGGAGACATGCTCCCAT  
TGTGGGGGACATTAGCAACATCACTCAGAAGCCCTGTGTTCTTCAAGAGCAGGTGTCTCAGCCTCATGTCCTCT  
GCGTGTCTGCACTCAGGACTGAAGTGTCTTAAAGCAAGGAGCTGTGAGAAGGAGCACTCCATGCTGTGCTGGGA  
GAATGGCTCTCACTACCTTTGCTCTTCAGTCTCCAGTGTCTTGGGTTTGTTTATACTTTGACAGCTTTTTTT  
AATTGTCATCATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACATTTTCCGCGAGGCCCTGGCAGGCGCA  
GGAATGCTCCAGCAGTGGCTCAGTGCTCCTGTGGTGTCTGAGCACTGGCATCTGGATGCTTAGCATGCAAGTT  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTGAGCTCCAGCTCCT  
TCTTGGTTGTCTAGTGTAGGTAGGCTATTTGGCCCCCTCTCTTATACCCATAAACCTTTCTACACTAGTGCCCA  
TGGGAACCAAGGCTGTAAAGATAGAGAGAGTGAAGATAGAGTCTGGAAGATAGCTGTCTATAACTGAGACTAGA  
CGGAAAGGAATACTCGTGTATTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCTTTTGGATGGATGTTGTGTGACAGAGCTGCTACAGACTGTACTAACACCGTAATTTGGCATTTGTTTAACT  
CTATTTTATAAAGCTTCAA AAAACCCCA

## **FIGURE 14**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624  
><subunit 1 of 1, 310 aa, 1 stop  
><MW: 35020, pI: 7.90, NX(S/T): 3  
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIIGGIIG  
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

# FIGURE 15

CAGGACACAGGTCCTCTACGCTGGAGCAGCGGGGAGACAGCCACCATGACACATCCTCGTGGTCCATGCCATGGTG  
ATCCTGCTGACGCTGGGCCCGCTCTCGAGCCGACGACAGCGAGTTCAGGCGCTGCTGGACATCTGGTTTCCGGAG  
GAGAAGCCATCGCCACCGCCTTCTGGTGGACATCTCGAGGAGGCGCTGCTGCTCTCTGACTGGCTGAAGCTG  
CGCATAGTCGTTCTGAGGTGCTCGCCTGGTGGACGCGCGCCTGACAGGACCTGGAGCGCGACGACAGGCGCA  
TTCGTGCGATCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCTCCAGTTCTCTGGACCAGGCAGTGGCCCCAC  
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC  
GGCGCCTCCGGAGGCGAGACTTTCACCTCTTGTCTCACAGCTCTCCCTGCGCCCCCGCCAGACAGCACAGAGGCA  
CCCAAACCAAAGAGCAGCCCCAGAGCAGCCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTG  
GGCCCTGAGGACGACCTGGCTGGCATGTTCTCTCCAGATTTCCTCCGCTCAGCCCCGGACCCCTCGGTGGCAGAGCTCC  
AGTCCCCGCCCTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCCGCTCGTCCAGGGCAGCCCC  
GAGGTGCGGGGCATCACGGTGGCTGTCTGCAGGCCCTCGCCACCCCTGCTCAGCTCCCCACAGCGCGGTGCCTTG  
GTGATGTCCATGCACCGTAGCCACTTCTCTGGCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG  
CCACAGGACACCGGCTTCTCCTCGCTCTTCTGAAAGGTGCTCCTGACAGATGCTGCAGTGGCTGGACAGCCCTGGC  
GTGGAGGGCGGGCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCTCAGCCGGCGCGAGGCTCAGTGAT  
GTGCGAGGGGGCTCTCTGCGCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTTCAGCTCCACCGTC  
CGTGCCGTGTCATCGCCACCTGAGGCTCTGGGGAGCAGTGCAGCGTGGAGCGCGGACCTGCATCAGCAAAGTCTCCAG  
GGGCTGATCAGGTGAGGTCTCCCCACCTGGAGGAGCTGCTGACTGCATTCTCTCTGCCATCGCGGATGCTGCC  
TCCCGCTTTCAGGCTGTAAAGCCCGTTGTGGTGGTGGAGCTCCCTGCTGCTGTCAGGAGGAGGAGCCCCCTGGCTGGG  
GGGAAGCCGGGTGCGGACGCTGGCAGCTTGGAGGCCGTGGCGCTGGGGCCCTGTCAGGCCCTCTGAGGCTCTGAGTGG  
CTGGAAATGCTGGACCCCGAGGTGGTGCAGAGCTGCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGAGGGAAG  
GGCAAAGGTGAGGCCAGGTGGCCCTCGTTCGGTCCCTACCTCTGACCCCTCTTCACGCATCAGTCCAGCTGGCCC  
ACACTGCACCAAGTGATCCGAGTCTGTCTGGGCAAGAGCCGGGAACAGAGGTTTCGACCCCTCTGCGCTCTCTGGAC  
TTCCTCTGGGCTGCATCCATGTTCTCTCGCATCTGGCAGGGGCGGGACCAAGCGCACCCCGCAGAAGCGCGCGGAG  
GAGCTGCTGCTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCTTGGCCGAGGCGGAGACGCGG  
AGCCAGGACGGGGACACAGCCGCTTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG  
GACGATGAGAGTGTGAGGAAGGTGACGGAGCACTGTGAGGCTGCATCAGCAGTGGGAGGACAGCGTGTGGGA  
AGGCGCTGCCGAGACCTTCTCTGAGCTCTACCTACAGCGGCCGAGCTGCGGGTGGCCGTGCTGAGTGGCTCTA  
CTGCACAGCGAAGGGGCTGCCAGCAGCAGCTGTGCAAGCTGGACGGACTCATCCACCGCTTCATCAGCTGCTCTT  
GCGGACACCGAGACTCCCGGGCGTGTGGAGAACCGAGGGCGGATGCCAGTGGCTGCGCGGAGCTGGCGGTG  
GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCTCTGTCAGCGCCGACCCCACTCAACTTC  
CAGGAGTTCGGGCGAGAGAACCACTGAGCTGCTTCTGTCAGCTGCTGGGCCCTGCTGGAGCTGCTGCAGCCGAC  
GTGTTCCGCGAGCAGCACAGGGGGCGCTGTGGGACTGCCTTCTGTCCTTCACTCCGCTGCTGCTGAATTACAG  
AAGTCTCCCGCGCATCTGGCTGCCTTCAACAAGTTTGTGACGTTAGTCCATTAAGTACATTACCTACAATGCC  
CCAGCAGCCATCTCCTTCTGAGAACGACGCGGACCCGCTCCACGACCTGCTCTCGACAACAGTGACCTGGTG  
ATGCTGAAATCCCTCTTCTCAGGGCTCAGCTGCCCCAGCAGGGACGACGAGCCGACCGAGGCTGGACGAAGAG  
GGCGAGGAGGAGCTCAGCGGCTCCCTTGGCCCTGGTCAAGCTCTCCCTGTTCAACCTCTGACCGCGGCGGAG  
ATGGCCCCCTACATGAACCGGCTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC  
GAGATGTCCCGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG  
GAGTGTTCGCGCAACTCTCGCTTACGCTGGCCCTGCGCTCCATGCAGAACAGCCCGAGCATTGCAGCGCTTTC  
CTGCCACGTTTCATGTACTGCTGGGCGAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCTGAG  
TACGCTCTCTGTGCCAAGAGCAGCGGCTGTGCTGCTCCACCGGGCCTTCTGGTGGGCATGTACGGCCAGATG  
GACCCAGCGCGAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCTGTGGCAGCCGA  
CCCCCTCCAAGCCCGGCCGCTCCGCTCCCGGGGATCCTCGAGGCAAGCCAGGAAGCTGGGCGTGTGCTGG  
TCTGTCCGAGGAGGTGAGGCGCCGAGCCCTGAGGCCAGGCGAGGCCAGAGCAATCTCCGAGCCCTGGGGTGG  
CTCGGGCGGGCGCTGGCATCAGGGGCGCTCCAGCAAGCCCTCATTCACCTCTTGGGCCAGCCCTGCCGCGG  
AGCGCGGATCCCCCGGCATGGCTGGGTGGTTTTGAATGAACGACCTGAAGTGTCAA

1032690.12731

## FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRM  
IRSEVLRRLVDAALQDLEPQQLLLFVQSFQIPVSSMSKLLQFLDQAVAHDPQTLEQNIIMDKNY  
MAHLVEVQHERGASGGQTFHSLLTASLPFRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG  
PEDDLAGMFLQIFPLSPDRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL  
ATLLSSPHGGALVMSMRSHFLACPLLRQLCQYQRCVPQDTGFSSFLFKVLLQMLQWLDSFG  
VEGGPLRAQLRLASQASAGRRLSDVRGGLRLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ  
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASFPACKPVVVVSSLLQEEEP  
GGKPGADGGSLEAVRLGFPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGAQVPSFR  
PYLLTLFTHQSSWPTLHQCIRVLLGKSREQRFDPASLDLWACIHVPRIWQGRDQRTQPQR  
REELVLRVQGPELISLVELILAEATRSDGDTAACSLIQARLPILLSCCCGDDSVRKVTE  
HLSGCIQQWGD SVLGRRCRDLLQLYLQRPRLVPVPPEVLLHSEGAASSSVCKLDGLIHRFI  
TLADTSDSRALENRGADAMACRKLAVAHPLLLLRHLPMIAALLHGRTHLNFQEFRRQNH  
SCFLHVLGELLEQLPHVFRSEHQGALWDCLLSFIRLLNRYKSSRHAAFINKFVQFIHKYI  
TYNAPAAISFLQKHADPLHDLSFDNSDLVMLKSLLAGLSLPSRDRDTRGLDEEGEEESSAG  
SLPLSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSRRRPEILSFFSTNLQRL  
MSSAECCRNLAFLSLALRSMQNSPSIAAFLPTFMYCLGSDQDFEVVQTALRNLPEYALLCQE  
HAAVLLHRAFLVGMYGQMDPSAQISEALRIHMEAVM

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

#### **N-myristoylation sites.**

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,  
665-671, 698-704

#### **Amidation sites.**

amino acids 329-333, 634-638



## FIGURE 17

CCGGGCCATGCAGCCTCGGCCCGCGGGCGCCCGCGCACCCGAGGAGATGAGGCTCCGC  
AATGGCACCTTCTGACGCTGCTGCTTCTGCTGTGCGCCTTCTCTCGCTGCTGCTGGTA  
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCCTGGCGC  
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG  
GTGCTGGACGAGATCAAGAGGGCCGTGTCAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA  
TCGCACCTGGGCGCGCTTAACAGAGGACCCCGATTGAAGCCGTGGAAACGGCTCACACCGGC  
ACGTGCTGCACCTGCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT  
CTGCAGCCCGCGGTGCGCGTGGGCGAGGCGCGCACCGGAGTGTCGTTGGTGATGGGCATCCC  
GAGCGTGCGGCGCGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC  
TGAGCCCGCAGGAGAAGGAGGACTCGGTATCTGTTGGTGTATCGCCGAGACTGACTCACAG  
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCT  
CCTGGAGGTATCTCACCTCCCCCACTTCTACCTGACTTCTCCGCTCCGAGAGTCTCT  
TTGGGGACCCCAAGGAGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCTCT  
ATGATGTACGCGCAGTCCAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA  
GCCCAACTACCTGAGCACCATTGAAGAACTTTGCACTGCAGCAGCTTCAGAGGACTGGATGA  
TCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG  
ATTGTAGAGTTCTATTCTCATGTTCTACCGGACAAGCCCATCGACTGGCTCCTGGACCATAT  
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA  
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCT  
GGCAAGATCCAGAAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT  
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATACCAGCACTTCACCCTGGAGAAAG  
CCTACCTGCGCGAGGACTTCTTCTGGGCTTCACCCCTGCCGCGGGGGACTTCATCCGCTTC  
CGCTTCTTCAAACCTTAAGACTGGAGCGGTTCTTCTCCGCACTGGGAACATCGAGCACCC  
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGTCGCTTCGACAACCTCAGTCAGACA  
AGGAGGCCCTGCAGGAGGGCGCACCGCCACCCTCCGGTACCTCGAGGCCCGACGGCTAC  
CTCCAGATCGGCTCCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC  
TCTGGAAGCACTGCGCTCTCGATCCAGACGGACTCCCTGTGTGGGTGATTCTGAGCGAGA  
TCTTCTGAAAAAGGCCGACTAAGCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCTGAA  
GCCACATTTCTGGGGGTGTCTGCTCACTGCGTCCCGGAGGGGCCAGATACGGCCCCGCCCAA  
AGGGTTCTGCCTGGCGTGGGGCTTGGGCCGGCCTGGGGTCCGCCGCTGGCCCGAGGCCCTA  
GGAGCTGGTGCTGCCCCCGCCGCGGGCGCGGAGGAGGAGGCGGCCCCACACTGTGCC  
TGAGGCCCGGAACCGTTTCGCACCCGCGCTGCCCCAGTCAGGCCGTTTATAGAAGAGCTTTTAC  
TTGGCGCGCCCGCTCTCTGGCGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT  
TTTATCTTGGATACATTTGATTTTTTTCACGTAAGTCCACATATACTTTATATAAGAGCGTG  
ACTTGTAAATAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

1003390.12701

## FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLTLLFLCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRHLHAAEQESLKRSK  
ELNLVLDEIKRAVSEKQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA  
KESSLQPAVRVGGQRTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE  
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLESFGDPKERVVRWTKQNLD  
YCFLLMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL  
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFFQHVGT  
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD  
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPPDNPQSDKEALQEGRTATLRYPRS  
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

### **Important features:**

#### **Signal sequence**

amino acids 1-23

#### **N-glycosylation sites.**

amino acids 5-9, 87-91, 103-107, 465-469

#### **N-myristoylation sites.**

amino acids 6-12, 136-142, 370-376, 509-515